1638

BIOTECHNOLOGY
SYSTEMS
BRANCH

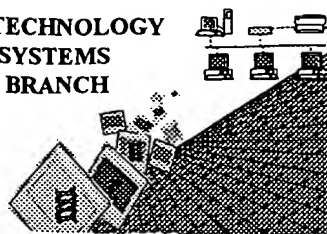# RAW SEQUENCE LISTING
ERROR REPORT

RECEIVED

OCT 0 7 2002

TECH CENTER 1600/2900

#19

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _09/646,532_

Source: _/600_

Date Processed by STIC: _10/1/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
    APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
    NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: **patin3help@uspto.gov** or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
     http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**, EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
   Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
            Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
   2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
   Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _09/646,532_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length

Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences
(OLD RULES)

Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences
(NEW RULES)

Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220>

Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

1600

```
RAW SEQUENCE LISTING                     DATE: 10/01/2002
PATENT APPLICATION:  US/09/646,532       TIME: 16:56:13

        Input Set : A:\Sequence Listing.txt
        Output Set: N:\CRF4\10012002\I646532.raw

   3 <110> APPLICANT: The Victoria University of Manchester
   4        Emes, Michael, James
   5        Tetlow, Ian, Joseph
   6        Bowsher, Caroline, Grace
   8 <120> TITLE OF INVENTION: TRANSPORTER PROTEIN
  10 <130> FILE REFERENCE: D088125PWO
  12 <140> CURRENT APPLICATION NUMBER: US 09/646,532
  13 <141> CURRENT FILING DATE: 2000-10-03
  15 <160> NUMBER OF SEQ ID NOS: 7
  17 <170> SOFTWARE: PatentIn Ver. 2.0


ERRORED SEQUENCES

  19 <210> SEQ ID NO: 1
  20 <211> LENGTH: 10
  21 <212> TYPE: PRT
  22 <213> ORGANISM: Wheat
  24 <400> SEQUENCE: 1
  25 Ser Met Pro Leu Asn Ala Ala Val Lys Met
E--> 26   1            5    5          10
  29 <210> SEQ ID NO: 2
  30 <211> LENGTH: 14
  31 <212> TYPE: PRT
  32 <213> ORGANISM: Wheat
  34 <400> SEQUENCE: 2
E--> 35 Gly Ala Xaa Xaa Xaa Glu Thr Ala Trp Ala Cys Gly Xaa Ala
E--> 36   1            5    5          10
  39 <210> SEQ ID NO: 3
  40 <211> LENGTH: 9
  41 <212> TYPE: PRT
  42 <213> ORGANISM: Wheat
  44 <400> SEQUENCE: 3
E--> 45 Asn Phe Arg Tyr Thr Asn Phe Ala Xaa
E--> 46   1            5    5
  49 <210> SEQ ID NO: 4
  50 <211> LENGTH: 12
  51 <212> TYPE: PRT
  52 <213> ORGANISM: Wheat
  54 <400> SEQUENCE: 4
E--> 55 Gly Ala Thr Xaa Gly Asn Xaa Ala His Ala Met Gly
E--> 56   1            5    5          10
  59 <210> SEQ ID NO: 5
```

Does Not Comply
Corrected Diskette Needed

pp 1-3

(global error)
10 misaligned numbers - see item 3 on Error Summary Sheet

see p.3 for error explanation

also,

p.3

p.3

misaligned nos.

10 misaligned nos.

```
        60 <211> LENGTH: 15
        61 <212> TYPE: PRT
        62 <213> ORGANISM: Wheat
        64 <400> SEQUENCE: 5
E--> 65 Ser Val Leu Trp Thr Glu Xaa Xaa Asp Xaa Xaa Xaa Gly Phe Arg
E--> 66   1               5    5            10        10      15
        69 <210> SEQ ID NO: 6
        70 <211> LENGTH: 8
        71 <212> TYPE: PRT
        72 <213> ORGANISM: Wheat
        74 <400> SEQUENCE: 6
E--> 75 Val Xaa Leu Ala Pro Xaa Asn Pro
E--> 76   1               5    5
        79 <210> SEQ ID NO: 7
        80 <211> LENGTH: 10
        81 <212> TYPE: PRT
        82 <213> ORGANISM: Wheat
        84 <400> SEQUENCE: 7
E--> 85 Pro Tyr Asn Xaa Ala Tyr Gln Asp Xaa Gly
E--> 86   1           5    5            10
```

(handwritten annotations: "p.3", "misaligned nos." appearing three times; various numbers "5", "10", "15" circled and marked)

VARIABLE LOCATION SUMMARY   DATE: 10/01/2002
PATENT APPLICATION: US/09/646,532   TIME: 16:56:14

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\10012002\I646532.raw

Use of n's or Xaa's(NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:2; Xaa Pos. 3,4,5,13
Seq#:3; Xaa Pos. 9
Seq#:4; Xaa Pos. 4,7
Seq#:5; Xaa Pos. 7,8,10,11,12
Seq#:6; Xaa Pos. 2,6
Seq#:7; Xaa Pos. 4,9

VERIFICATION SUMMARY　　　　　　　　　DATE: 10/01/2002
PATENT APPLICATION:　US/09/646,532　　　　TIME: 16:56:14

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF4\10012002\I646532.raw**

```
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:26 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:35 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
M:332 Repeated in SeqNo=2
L:45 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
M:332 Repeated in SeqNo=3
L:55 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
M:332 Repeated in SeqNo=4
L:65 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
M:332 Repeated in SeqNo=5
L:75 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
M:332 Repeated in SeqNo=6
L:85 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
M:332 Repeated in SeqNo=7
```